

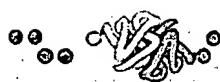


Search  for

as

# 1: AAC16476

LOCUS AAC16476 231 aa PLN 16-MAY-1998  
 DEFINITION putative acyl-CoA:cholesterol acyltransferase.  
 ACCESSION AAC16476  
 PID g3135276  
 VERSION AAC16476.1 GI:3135276  
 DBSOURCE locus ATAC003058 accession [AC003058.1](#)  
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 ORGANISM Arabidopsis thaliana  
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 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core  
 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
 Arabidopsis.  
 REFERENCE 1 (residues 1 to 231)  
 AUTHORS Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C.,  
 Sykes, S.M., Kaul, S., Mason, T.M., Kerlavage, A.R., Adams, M.D.,  
 Somerville, C.R. and Venter, J.C.  
 TITLE Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence  
 JOURNAL Unpublished  
 REFERENCE 2 (residues 1 to 231)  
 AUTHORS Rounsley, S.D. and Lin, X.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-NOV-1997) The Institute for Genomic Research, 9712  
 Medical Center Dr, Rockville, MD 20850, USA, rounsley@tigr.org  
 REFERENCE 3 (residues 1 to 231)  
 AUTHORS Rounsley, S.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-MAY-1998) The Institute for Genomic Research, 9712  
 Medical Center Dr., Rockville, MD 20850, USA  
 COMMENT Method: conceptual translation.  
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 121 llyaiervlk lsvpnlyvwl cmfycffhlw lnlaellcf gdrefykdwv naksvgydwr  
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Search  for

as

**1: AAC63997 ACAT related gene product 1 [Homo sapiens]**

LOCUS AAC63997 488 aa PRI 15-OCT-1998  
 DEFINITION ACAT related gene product 1 [Homo sapiens].  
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 PID g3746533  
 VERSION AAC63997.1 GI:3746533  
 DBSOURCE locus AF059202 accession [AF059202.1](#)  
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (residues 1 to 488)  
 AUTHORS Oelkers, P., Behari, A., Cromley, D., Billheimer, J.T. and Sturley, S.L.  
 TITLE Characterization of two human genes encoding acyl coenzyme  
 A:cholesterol acyltransferase-related enzymes  
 JOURNAL J. Biol. Chem. 273 (41), 26765-26771 (1998)  
 MEDLINE [98434592](#)  
 REFERENCE 2 (residues 1 to 488)  
 AUTHORS Oelkers, P., Cromley, D., Behari, A., Billheimer, J.T. and Sturley, S.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-APR-1998) Human Nutrition, Columbia University, 630  
 W. 168th Street, New York, NY 10032, USA  
 COMMENT Method: conceptual translation.  
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**ORIGIN**

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Search  for

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 PID g3859934  
 VERSION AAC72917.1 GI:3859934  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (residues 1 to 498)  
 AUTHORS Cases, S., Smith, S.J., Zheng, Y.-W., Myers, H.M., Lear, S.R., Sande, E.,  
 Novak, S., Collins, C., Welch, C.B., Lusi, A.J., Erickson, S.K. and  
 Farese, R.V. Jr.  
 TITLE Identification of a gene encoding an acyl CoA:diacylglycerol  
 acyltransferase, a key enzyme in triacylglycerol synthesis  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13018-13023 (1998)  
 MEDLINE 99007259  
 REFERENCE 2 (residues 1 to 498)  
 AUTHORS Farese, R.V. Jr.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-1998) Gladstone Institute, 2550 23rd Street, San  
 Francisco, CA 94110, USA  
 COMMENT Method: conceptual translation supplied by author.  
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 241 kkvsaaaaq avsydpnlty rdlyyfifap tlcylfnfpr sprirkrfl rrvlemlfft  
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as

1: CAB44774 diacylglycerol O-acyltransferase [Arabidopsis thaliana]

LOCUS CAB44774 520 aa PLN 10-JUN-1999  
 DEFINITION diacylglycerol O-acyltransferase [Arabidopsis thaliana].  
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 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (residues 1 to 520)  
 AUTHORS Hobbs,D.H., Lu,C. and Hills,M.J.  
 TITLE Cloning of a cDNA encoding diacylglycerol acyltransferase from  
 Arabidopsis thaliana and its functional expression  
 JOURNAL FEBS Lett. 452 (3), 145-149 (1999)  
 MEDLINE [99313150](#)  
 REFERENCE 2 (residues 1 to 520)  
 AUTHORS Hills,M.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-DEC-1998) Hills M.J., Department of Brassica and  
 Oilseeds Research, John Innes Centre, Colney Lane, Norwich, NR4  
 7UH, U.K

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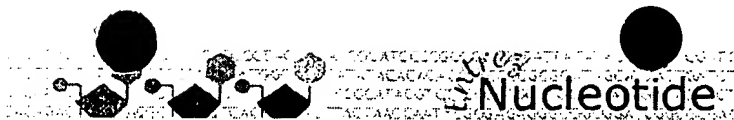


Search  for

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1: AAD45536 putative diacylglycerol acyltransferase [Brassica napus]

LOCUS AF164434\_1 503 aa PLN 30-NOV-1999  
 DEFINITION putative diacylglycerol acyltransferase [Brassica napus].  
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 PID g5579408  
 VERSION AAD45536.1 GI:5579408  
 DBSOURCE locus AF164434 accession AF164434.1  
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 ORGANISM Brassica napus  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (residues 1 to 503)  
 AUTHORS Nykiforuk, C.L., Laroche, A. and Weselake, R.J.  
 TITLE Isolation and Characterization of a cDNA Encoding a Second Putative  
 Diacylglycerol Acyltransferase from a Microspore-derived Cell  
 Suspension Culture of Brassica napus L. cv Jet Neuf (Accession No.  
 AF164434). (PGR99-158)  
 JOURNAL Plant Physiol. 121 (3), 1053 (1999)  
 REFERENCE 2 (residues 1 to 503)  
 AUTHORS Nykiforuk, C.L., Laroche, A. and Weselake, R.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-JUN-1999) Chemistry and Biochemistry, University of  
 Lethbridge, 4401 University Drive, Lethbridge, Alberta T1K 3M4,  
 Canada  
 COMMENT Method: conceptual translation supplied by author.  
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 121 lcvvvlvavn srliienlmk ygwliirtfdw fsstslrdwp lfmccslslv fplaaftvek  
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 481 ifgqpmcgll yyhdlmnrkg sms  
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Search  for

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1: AC003058

LOCUS ATAC003058 97495 bp DNA PLN 16-MAY-1998  
DEFINITION Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence.  
ACCESSION AC003058  
VERSION AC003058.1 GI:3135250  
KEYWORDS HTG.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 97495)  
AUTHORS Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Sykes, S.M., Kaul, S., Mason, T.M., Kerlavage, A.R., Adams, M.D., Somerville, C.R. and Venter, J.C.  
TITLE Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 97495)  
AUTHORS Rounsley, S.D. and Lin, X.  
TITLE Direct Submission  
JOURNAL Submitted (06-NOV-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rounsley@tigr.org  
REFERENCE 3 (bases 1 to 97495)  
AUTHORS Rounsley, S.D.  
TITLE Direct Submission  
JOURNAL Submitted (16-MAY-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA  
COMMENT [WARNING] On Dec 17, 1999 this sequence was replaced by a newer version gi:[6598388](#).  
On May 16, 1998 this sequence version replaced gi:[3128164](#).  
Address all correspondence to:  
Steve Rounsley  
The Institute for Genomic Research  
9712 Medical Center Dr,  
Rockville, MD 20850,  
USA  
e-mail: rounsley@tigr.org  
BAC clone F27F23 is from Arabidopsis chromosome II and is contained in the YAC clone CIC06E08.  
The orientation of the sequence is from SP6 to T7 end of the BAC clone.  
Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, <http://gnomic.stanford.edu/~chris/GENSCANW.html>), and NetPlantGene (<http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html>), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (<http://www.tigr.org/tdb/at/at.html>).  
Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins.

Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by repeatmasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Regions of genomic sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.

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IALIGYCHEGDQMALIYEYIGNGTLDGDLGSKNSSILSWEERLQISLDAAGLEYLHN  
GCKPPIVHRDVKPTNILINEKLQAKIADFGLSRSTLEGDSQVSTEVAGTIGYLDPEH  
YSMQQFSEKSDVYSFGVVLEVITGQPVISRSRTEENRHISDRVSLMLSKGDIKSIVD  
PKLGERFNAGLAWKITEVALACASESTKTRLTMSQVVAELKESLCRARTSGDSGDISF  
SEPTEMNVSMSTVDPGVLPQPR"



repeat region complement(11138..11160)  
/rpt\_family="AT\_rich"

misc feature complement(12886..12925)  
/note="exon predicted by xgrail, quality good"

mRNA complement(join(<13430..13585,13844..15762,  
16010..16186,16516..16604,16763..>16944))  
/gene="F27F23.4"

gene complement(<13430..>16944)  
/gene="F27F23.4"  
/note="predicted by genscan"

CDS complement(join(13430..13585,13844..15762,16010..16186,  
16516..16604,16763..16944))  
/gene="F27F23.4"  
/note="hypothetical protein"  
/codon\_start=1  
/protein\_id="AAC16454.1"  
/db\_xref="GI:3135254"  
/translation="MAPSEIEPALQEPGSLVLSREDRRFANLRGVRWRVNLGVLP  
ASSIDEFRRRAANSRRRRRLMDPHVLKHEDSSPNFIIDNPLSQNPNSTWGQFFRNAE  
LEKTLDDQLSRLYPEHWCFYQTPRYQGMRLRILLWCLKHPEYGYRQGMHELLAPLLY  
VLHVDIMRLSEVRKSYEDYFTDRFDSLSFMERDITYTFDFNKFMDSDVNDGIGSQGH  
SKNFNSLDELDPVQSLVMLTDSYGTESELGIVLSEKFMHEDAYCMFDALMSGIHGCFAM  
ASFFSYSPASGSHTGLTPVLEACSAFYRILAVVDSSLHSHLVELGVPEQYFGLRWLRV  
LFGREFLLQDLLLVWDEIILADNSARTDEDSRNQNFRIIFDCPRGTLVLGMTVSMILYL  
RSSLLSTENATCCLQRLNFPENIDLNKIIQAKLLQALVLDTDMLSALSINGVFDQS  
NFVPARTKSCSTSPRSPLIIAPESYWEKKWRVLHKAEEEEENKICLEKQTPPTQKKRW  
LNVTKLFRVIDLSHHKLGIGERKANSSPVTQSLLEDSSQLNVDCHVTNKENIHPQ  
ETEENIMEFHSADEESIVSGSSPSEESSFVSLDPTSPVRCSTKIENDSVSSAGSNLLP  
DEDDKSIVSISEENSSVSDPISPAIDSNYSKYLDCTGSENDKQDQTSVNSPLSVS  
PHRRNEYPVTQSDQSDVSTDKSVGITKEYKLLHGIVQWFRKLKRTLSSSEETSHRKASDA  
TKTNDVKIKKNQIGCYSESHQALSSGDSSQNLRLKTLKNLGQSMMLKHIEAIELVFQQE  
PCLVPAGLIGNLAKTNLIEKGQVTATTALKELRKL SNLLSEM"

mRNA join(<17068..17148,18012..18127,18236..18341,  
18392..>18550)  
/gene="F27F23.5"

gene <17068..>18550  
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CDS join(17068..17148,18012..18127,18236..18341,18392..18550)  
/gene="F27F23.5"  
/codon\_start=1  
/product="Mg-chelatase subunit D-like protein"  
/protein\_id="AAC16455.1"  
/db\_xref="GI:3135255"  
/translation="MNDDENMFVCCVRDSRREEPIDEEEQSYRCLILNIVEREGIS  
FRNPCKPLLVAIYQPEEGAIQDFEDPVAAVGIAKQLQEHCEVFRMVKETNSNEHCNV  
KLVSILVLKCYSMTMWISLKMTRLRMVIMILKRRKTEIALVAWEMLAMKMAT"

repeat region complement(17380..17504)  
/rpt\_family="(TAAA)n"

misc feature 18632..18706  
/note="exon predicted by xgrail, quality good"

misc feature 19078..19123  
/note="exon predicted by xgrail, quality marginal"

misc feature 19480..19517  
/note="exon predicted by xgrail, quality marginal"

misc feature 19557..19652  
/note="exon predicted by xgrail, quality excellent"

misc feature 19737..19810  
/note="exon predicted by xgrail, quality marginal"

misc feature 19935..20056  
/note="exon predicted by xgrail, quality marginal"

misc feature complement(20075..20092)  
/note="exon predicted by xgrail, quality  
marginal\_shadowexon"

repeat region complement(20457..20499)  
/rpt\_family="AT\_rich"

repeat region 20531..20576  
/rpt\_family="(GA)n"

repeat region complement(20700..20787)  
/rpt\_family="(CAAAA)n"

misc feature 21345..21442  
/note="exon predicted by xgrail, quality good"

misc feature complement(21512..21553)  
/note="exon predicted by xgrail, quality marginal\_shadowexon"

misc feature 21590..21671  
/note="exon predicted by xgrail, quality excellent"

mRNA join(<21713..23229,23377..23431,23522..23625,23778..23868,23909..23941,24091..24215,24233..>24269)  
/gene="F27F23.6"

gene <21713..>24269  
/gene="F27F23.6"

CDS /note="predicted by genscan"  
join(21713..23229,23377..23431,23522..23625,23778..23868,23909..23941,24091..24215,24233..24269)  
/gene="F27F23.6"  
/note="hypothetical protein"  
/codon\_start=1  
/protein\_id="AAC16456.1"  
/db\_xref="GI:3135256"  
/translation="MLVESSFSSSVETSLNLVSEYQDPFAAYDWTSLAESYQMIHKVPEQSQVSFLKNVPVTDTMNLDESKHPKHQESCSEKSVMHKVSQKALTSVYRRRKRTLI  
PGGTEEHNLGKIRKQDDSLDDSIYSLYNPEESTKRKNRFNNCLVYSRKKRRGESSCTF  
TGETTIRGDGLDDAFVSEHDCGETRRRGNRSDCLVYSRKKGRVKFNCSFSKHVTGR  
TKISYDQADSSACSQMGQIVKADSSLTRPKPGEIKKSGHQLVYSQRKQLVKSNGSFTE  
SHVGKTKRNGDRSEVLLTYSRRKSGKSGIVRVNGFLVYTRKKLFRGPFARRDLSET  
KKNQDQRSTVSSRELLDDTQVTEVTCSSDGTNDSCSLKSSSEVNSTSSKSREDDCYS  
SDSGVSETDTDGSSSPFRQCKHCDKPGTVEKMLICDECEEAYHTRCCGVQMKDVAEID  
EWLCPSCLNQSSKTKTKGRISHERKWRVTVPFVIGIRIGKMFQADVPDWGPTMSDT  
SFVGEPLIEIGQSEYMHDLLKAKNSKKQCSAVNWLQCREEDTNGVICGWRRAPRSEVQ  
TKDWECFCCFSWDPSRADCAVPQKNPSEDEKLAAELETSEILKQLKYIKMVRYSHYL  
FDLSRPYSFLIKDLKLRLDLDTQPKSEN"

misc feature complement(24507..24590)  
/note="exon predicted by xgrail, quality good\_shadowexon"

mRNA complement(join(<24731..24895,25375..>26289))  
/gene="F27F23.7"

gene complement(<24731..>26289)  
/gene="F27F23.7"

CDS complement(join(24731..24895,25375..26289))  
/gene="F27F23.7"  
/note="unknown protein"  
/codon\_start=1  
/protein\_id="AAC16457.1"  
/db\_xref="GI:3135257"  
/translation="MDSLVAASYASSDEEEDLQPRREAFTVKSSEPSASSLFSAPQPK  
ELKSSDGDGSSSSRGKSSSFLSSLPKSSISRKKNPNPSSIPKRQVQIRLPVNPR  
PSNLDDDEDEEEKARKKRKQMESASASHDSSVRSFLSAMPAPKSSQTLGALPSLGSG  
SGRRSNLETETPSIAFPQTDSGISDQQNQSYESFSHSNSETQIVGVNDNYATGYDGG  
YETIPSGSSVGYGSSYGNTWNGGGFEAMTGLPEAVVAMDSGARRGRGRNQMPPIV  
EVKQDELKMNRPVVDQVKSTGIAFGPAYQPVTSSSKGVSKLHKRKHQITALFMDMKH  
KESELTERRSRGLLTKAETQAKYGW"

repeat region complement(25930..25971)  
/rpt\_family="(GAA)n"

repeat region 26293..26327  
/rpt\_family="(GA)n"

mRNA <27054..>29135  
/gene="F27F23.8"

gene <27054..>29135  
/gene="F27F23.8"

CDS 27054..29135  
/gene="F27F23.8"

CDS

/gene="F27F23.11"  
/codon\_start=1  
/product="putative 18.5 KDa class I heat shock protein"  
/protein\_id="AAC16461.1"  
/db\_xref="GI:3135261"  
/translation="MSMIPISNRRRLSPGDRIWEPPFELMNTFLDFPSPALFLSHHFPS  
LSREIFPQTSSSTVNTQLNWTETPTAHVFKAYLPGVDQDEVIAFVDEEGYLQICTGDN  
KFMSRFKLPNNALTDQVTAWMEDEFLVVFVEKDASSSPQLPEIEENRNVRVVEITGD  
DD"  
mRNA complement(<35246..>35479)  
/gene="F27F23.12"  
gene complement(<35246..>35479)  
/gene="F27F23.12"  
/note="predicted by genefinder"  
CDS complement(35246..35479)  
/gene="F27F23.12"  
/note="hypothetical protein"  
/codon\_start=1  
/protein\_id="AAC16462.1"  
/db\_xref="GI:3135262"  
/translation="MEATKERMEKDQKKRVVTNEAGKAEDNTIRTIIRESIVEDRGSN  
DDGDKNDNDHGASKPEDILAFSRTVVRKIDSSLE"  
repeat region complement(35434..35502)  
/rpt\_family="(GA)n"  
misc feature 35505..35714  
/note="exon predicted by xgrail, quality good\_shadowexon"  
repeat region complement(35815..35856)  
/rpt\_family="AT-rich"  
repeat region complement(36232..36341)  
/rpt\_family="(TAAAA)n"  
repeat region complement(36645..36668)  
/rpt\_family="AT-rich"  
misc feature complement(36701..36723)  
/note="exon predicted by xgrail, quality  
excellent\_shadowexon"  
repeat region 37269..37319  
/rpt\_family="(TA)n"  
mRNA join(<37329..37616,37890..38059,38151..>38835)  
/gene="F27F23.13"  
gene <37329..>38835  
/gene="F27F23.13"  
/note="predicted by genscan"  
CDS join(37329..37616,37890..38059,38151..38835)  
/gene="F27F23.13"  
/note="hypothetical protein"  
/codon\_start=1  
/protein\_id="AAC16463.1"  
/db\_xref="GI:3135263"  
/translation="MICEEAYHQPPQIQKEQMMTMDQRNNHQKRSPSPSPSPSPSPS  
SPSPSPKSPSFNNNEERLEVVNLSGMALESIPNPSLNLAQICKLDLSNNHLQTIPESL  
TARLLNLIALDVHSNQIKALPNSIGCLSKLKTNLVSGNFLVSFPKSIQHCRSLEELNA  
NFNKLIRLPDSIGFELTNLRKLSINSNKLISLPISITHLTSRLVLDARLNCMLIPDD  
LENLINLEILNVSQNFQYLSALPSSIGLLMNLIELDVSYNKITVLPESIGCMRRLRKL  
SVEGNPLVSPPIEVMEQNLQVVREYLTQKMNGGSPRSPSKKKSFGKLVKYGTFNNG  
SRSWNREEREGFIMPEYRSIDSLASPRYSGMFSPRRLFSPTYFSR"  
repeat region 37393..37488  
/rpt\_family="(CAT)n"  
misc feature complement(39371..39466)  
/note="exon predicted by xgrail, quality  
marginal\_shadowexon"  
mRNA complement(<39656..40234)  
/gene="F27F23.14"  
gene complement(<39656..40234)  
/gene="F27F23.14"  
CDS complement(39656..40177)

/gene="F27F23.14"  
/note="unknown protein"  
/codon\_start=1  
/protein\_id="AAC16464.1"  
/db\_xref="GI:3135264"  
/translation="MAPRSDSQTGSSVSDGSDQSSMDPIFHLLRIVPFSFLRPPRLRL  
KIPSFITLPSMTVYALILLTYFLVVSFGFVYDVIVEPPGIGSTQDPTTGTIRPVVFMMSG  
RVNGQYIIIEGLSSGFVFLGGIGIVMLDLALDKNKAKSVKASYAVAGVSSIVIAVYMS  
MLFIRIKIPGYLY"  
misc feature 40515..40611  
/note="exon predicted by xgrail, quality good"  
mRNA join(40644..40900,41358..41621)  
/gene="F27F23.15"  
gene 40644..41621  
/gene="F27F23.15"  
CDS join(40711..40900,41358..41479)  
/gene="F27F23.15"  
/note="unknown protein"  
/codon\_start=1  
/protein\_id="AAC16465.1"  
/db\_xref="GI:3135265"  
/translation="MAYVDHAFSISDEDLDMIGTSYTVSNRPPVKEISLAVGLLVFGTL  
GIVLGFFMAYNRVGGDRGHGIFIVLGCLLFIPGFYYTRIAYYAYKGYKGFSSFNIPS  
V"  
misc feature complement(41924..42096)  
/note="exon predicted by xgrail, quality  
marginal\_shadowexon"  
misc feature 42333..42361  
/note="exon predicted by xgrail, quality marginal"  
repeat region complement(42840..42968)  
/rpt\_family="(TAAA)n"  
repeat region 42922..42978  
/rpt\_family="(TA)n"  
mRNA join(<43061..43198,43612..43854,45290..>45340)  
/gene="F27F23.16"  
gene <43061..>45340  
/gene="F27F23.16"  
/note="predicted by genscan"  
CDS join(43061..43198,43612..43854,45290..45340)  
/gene="F27F23.16"  
/note="hypothetical protein"  
/codon\_start=1  
/protein\_id="AAC16466.1"  
/db\_xref="GI:3135266"  
/translation="MANLIVLYILVIEAMIVIGSESSDSRDAEINRLKLNKPFLKS  
IKMRPTSYPEGWSNKSNDNEKHKMPQLWTINGKCPKNSIPIRTRKEDILRAKSIER  
FGKKDPNNIHQHKPTNPTNNDGTHEFKVETSLLIIPRKILS"  
misc feature complement(45387..45443)  
/note="exon predicted by xgrail, quality  
marginal\_shadowexon"  
repeat region 45508..45622  
/rpt\_family="(CAAAA)n"  
mRNA <46273..>46581  
/gene="F27F23.17"  
gene <46273..>46581  
/gene="F27F23.17"  
/note="predicted by genscan and genefinder"  
CDS 46273..46581  
/gene="F27F23.17"  
/note="hypothetical protein"  
/codon\_start=1  
/protein\_id="AAC16467.1"  
/db\_xref="GI:3135267"  
/translation="MERERGSERERERERERERERERERERERERERERERERE  
REREREREREREREREREKHKPATLAKNRRRRFVKNRRRRDHRRRISIIDGYESQF

"  
unsure 46294..46465  
/gene="F27F23.17"  
/note="Unable to sequence across the GA repeat region. The size of this region was estimated from the size of 6 shotgun clones."  
repeat region 46294..46413  
/rpt\_family="(GA)n"  
repeat region 46414..46467  
/rpt\_family="(GA)n"  
misc feature complement(46849..46920)  
/note="exon predicted by xgrail, quality marginal\_shadowexon"  
misc feature 46851..46892  
/note="exon predicted by xgrail, quality marginal"  
repeat region complement(46922..46960)  
/rpt\_family="AT-rich"  
misc feature 46982..47044  
/note="exon predicted by xgrail, quality good"  
misc feature 47142..47253  
/note="exon predicted by xgrail, quality excellent"  
misc feature complement(47175..47255)  
/note="exon predicted by xgrail, quality excellent\_shadowexon"  
misc feature 47605..47739  
/note="exon predicted by xgrail, quality excellent"  
repeat region 47884..47946  
/rpt\_family="(TAAAA)n"  
repeat region 47903..47946  
/rpt\_family="POLY\_A"  
mRNA join(<48238..48324,48412..48486,48584..48684,48805..49011,49139..49348,49825..50870,51499..51581,51712..51786,51899..52029,52237..52600,52694..52801,52901..>52963)  
/gene="F27F23.18"  
gene <48238..>52963  
/gene="F27F23.18"  
CDS join(48238..48324,48412..48486,48584..48684,48805..49011,49139..49348,49825..50870,51499..51581,51712..51786,51899..52029,52237..52600,52694..52801,52901..52963)  
/gene="F27F23.18"  
/codon\_start=1  
/product="putative RNA-binding protein"  
/protein\_id="AAC16468.1"  
/db\_xref="GI:3135268"  
/translation="MVWFQCDCCGENLKKPRLPRHMSMCTATKFSIDCGNMFGQVSV  
HYHNQCITEAEKYGPMVRSNGESSKQKHDFDINAELFNSQWFCSLCNATMTCEQDYFA  
HVGKKHQEKANEVADMDYSKQSEHPAVDKNNLTQQPDLDIYVGLSNDYPWFCSLCD  
INATSEQTLLAHANGKKHRVKVERFDAEQKQKQSTQHSTVDKKDYSKQQIEVDINVGL  
SNCYPWFCSLCNVKATCQONLLSHANGRKHRENVLFDATQQQOLEKTTVDDKDDTTVN  
ASDGNSEQKKVDLLVSSGVANGYSQAHKKRKLETCDETWKREVVQAEAKGGGEQKSE  
SKKAKKQDKEKKRKKDKKQTKSDSDFEHDKEDIKQLLVAYSKEELVNLIYKTAEKGSR  
LISAILESADRDIQRNIFVRGFGWDTTQENLKTAFESYGEIEECVVMKDKTGRGKG  
YGFVMFKTRKGAREALKRPEKRMYNRIVVCNLASEKPGKAGKEQDMAEPVNIDLTMA  
NQSEAVLPGIELGRGHVLEKMHQQQQTMDMFGQNMFPYGYSHQFPFGFDPYMGALSGN  
QMLAGLPNYDLNFDNRKTKKMVWFQCEDCGESLKKPKLSCIDCGEMFGRDTPVQGHNC  
ITEAEKYGPKGQSKSANGTPAKPKDISKQEPDFDINVGLSNRYPWFCSLCNTKATSQQ  
TLLAHADGKKHRGKAKAFHARQQQEQSTTLDNKDGSENASNVDSEQKKVDLPASSGVA  
NGESHPEKKRKLETLDDETSEGEAAKGSDDLKAKKQDHEKKINWKKLITSALKSNEDKT  
LKMKKLKLVLESIVDSGRDKSELKAELELVNLSSRFTVDGKYVKLVAKD"  
repeat region 50112..50214  
/rpt\_family="(GAAA)n"  
misc feature 54041..54119  
/note="exon predicted by xgrail, quality marginal\_shadowexon"

repeat region complement(54151..54181)  
/rpt\_family="(GAAA)n"  
misc feature 54192..54262  
/note="exon predicted by xgrail, quality marginal\_shadowexon"  
misc feature complement(54230..54255)  
/note="exon predicted by xgrail, quality marginal"  
repeat region 54297..54352  
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mRNA complement(join(<54518..55143,55234..55456,  
55563..55620,55718..55788,55988..56062,56160..56606,  
57088..57176,57259..57318,57413..57486,57616..58374,  
58538..58720,59316..59611,60133..60385,60462..>60859))  
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gene complement(<54518..>60859)  
/gene="F27F23.19"  
CDS complement(join(54518..55143,55234..55456,55563..55620,  
55718..55788,55988..56062,56160..56606,57088..57176,  
57259..57318,57413..57486,57616..58374,58538..58720,  
59316..59611,60133..60385,60462..60859))  
/gene="F27F23.19"  
/note="unknown protein"  
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/protein\_id="AAC16469.1"  
/db\_xref="GI:3135269"  
/translation="MSAPGKFDYSSGGLDRPLYRSNFAAQMERSSSFRESMEHPVPSH  
PIMLRTTSPIAQTDVTNFFQCLRFDPKVVAADHKSIHQGDFKRHVSIAGILGDES  
GSLKGFIPSPPIPEEIKRFKAGLRENNVKARERVKIFNEASSVFNKFFPSVPTKKRSR  
PEGFSGDRSGDRLVSGPGLGKMGIQGQTLAGGFELDQQLDERPKSGVPNKRTSMM  
DVRNNCIVRQSAAVDKDKEIMRVGNHNAVQGEDRTSTGIDGWETSKMKKKRSSINADC  
HPNLASNKVVDGYRDLKQGIQKPTGDSRSRVNGDSNMFRQSAGNGATGYGRSDSLSH  
QTSLAGHSPLARVDSHDNSLYSEKRERSIVSDKERVNLRGVNKSNIHDEFNSSSLVSN  
TKTNASVRGPRSGSGLPPKLSPLHNTSPSIEWDISGCTNKPPTLSGVTQKRMTSNR  
SSSPVPTQWASQRPQKISRIARRTNLVPIVSSQDEVPSYSDNISDVGCSETGFGFHKRS  
PAASPQLKLKGESSFSTAALSESEESGHPEIKSKDKGKQSDVDGKAAQNI PRVSIPA  
LQSRKSNKPAAGEEIGDGVRRQGRTRGRGFSSTRSLNPNPKNVKNVGTAKHLRSARPI  
FDKNERKLSDRKAYKQRATATNAPTLDHFVGSNDGREELLAAVNSAINIAQNFPNSF  
WKQMERYFGYISDDHINFLKQQELSSMGPTPVLTSSEFDSPVFPEELATSRADSKAS  
PLYQRLLSALISEDSDMGVNEDLQVDLDDDDSEFVSVLNNMEFNGFRNNERLELDESENDG  
SAILFKGVDKSAHCHNGKFPDNPIDFVDIQYDKLGIDEKIYLEAQSLGISIDLMP  
SNVEDEGIADIEIKKLEEAICNEGSKKKEIVDRLLKPAIEMKELQEKELDQGYEKLIE  
MAYEKSASRRHHNAGGKNSNNKISKQAALAFVRRTLERCHQFEKTGKSCFSEPEIKD  
MFIAGLATAEDTMDKEYNTSTSTPMGSGPSSSLALIGQNSSEYAKSSDVLPSENALL  
EQTTGKEDTAWSNRVKKRELLLDVVGIGTQLSSNTKGKRSRDRDRDGKGQASSRGGTNK  
IGRPSLSNAKGERKTKAKPKQKTTQISPSVRVPEQPKPSLPKPNEANSEYNNLEALEE  
TEPILDLSQLQIPDGLGDFDAQPGDINSWFNMDDDEEDFDMTELGIPTDDISELNIKL"  
misc feature 61108..61213  
/note="exon predicted by xgrail, quality marginal\_shadowexon"  
misc feature complement(62172..62289)  
/note="exon predicted by xgrail, quality excellent"  
repeat region 62692..62765  
/rpt\_family="AT-rich"  
repeat region complement(63242..63319)  
/rpt\_family="POLY\_A"  
repeat region 63477..63530  
/rpt\_family="(GAA)n"  
misc feature complement(63577..63664)  
/note="exon predicted by xgrail, quality marginal"  
misc feature complement(63905..63963)  
/note="exon predicted by xgrail, quality good"  
mRNA complement(join(<64017..64084,64176..64260,  
64265..64408,64479..64592,64677..64814,64993..65077,  
65273..65352,65478..65721,65801..66042,66131..66214,  
66302..66476,66685..>66863))

gene /gene=27F23.20"  
complement(<64017..>66863)  
/gene="F27F23.20"  
CDS complement(join(64017..64084,64176..64260,64265..64408,  
64479..64592,64677..64814,64993..65077,65273..65352,  
65478..65721,65801..66042,66131..66214,66302..66476,  
66685..66863))  
/gene="F27F23.20"  
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/product="putative protein kinase"  
/protein\_id="AAC16470.1"  
/db\_xref="GI:3135270"  
/translation="MENQEEDEVVLAKVTSEVEDNFEDEGLVSNSTLEKVAAAKKYIE  
NHYNRRMRHIQQRKERRWVLEQKIASLDVSEKEQLELLEDLQRKETETRLMRNRLCV  
DDFDLLSIIGRGAFGEVRLCREKKTGNIYAMKKLKKSEMLSRGQVEHVRAERNLLAEV  
ASDCIVKLYYSFQDPEYLYLIMEYLSGGDVMTLLMREETLTETVARFYIAQSVLAIES  
IHKHNYVHRDIKPDNLLLDKYGHMKLSDFGLCKPLDCRNISAMNVNEPLNDENINESI  
DGDENCISIGRRGRWKSPLQLQHWQINRRKLAYSTVGTPTYIAPEVLLKKGYGVECD  
WWSLGAIMYEMLVGYPFYSDDPVTTCKRIVSWRTHLVFPEGARLTPEARDLICRLLC  
DSEHRLGSHGAGAEQIKAHTWFKDVEWEKLYEMDAAFKPVVNGELDTQNFMKFDEVEC  
PKPARTGSGPSWKVLQFSGKSYIIISLIRGVLLCTYRSTGPLFLLVSITPQNINFGY  
TYRNFDAVRGSRHSLDIKGSVSPRSSTDSTRKSCY"  
repeat region complement(67208..67305)  
/rpt\_family="AT\_rich"  
repeat region 67324..67389  
/rpt\_family="AT\_rich"  
repeat region complement(67482..67596)  
/rpt\_family="(TAA)n"  
repeat region 67691..67736  
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repeat region 76796..76890  
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misc feature 78369..78552  
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repeat region 89470..89519  
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excellent\_shadowexon"  
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marginal\_shadowexon"  
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